```
CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT        48
Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
 1               5                  10                  15

AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG        96
Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
            20                  25                  30

GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA       144
Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
        35                  40                  45

CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA       192
Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
    50                  55                  60

TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA       240
Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
65                  70                  75                  80

GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC       288
Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
                85                  90                  95

ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG       336
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
            100                 105                 110

TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT       384
Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
        115                 120                 125

TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG       432
Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
    130                 135                 140

TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT       480
Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
145                 150                 155                 160

ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA       528
Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
                165                 170                 175

ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG       576
Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
            180                 185                 190

TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT       624
Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
        195                 200                 205

TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC       672
Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
    210                 215                 220

TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA       720
Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
225                 230                 235                 240
```

Figure 1

```
GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTATTTCC              768
Val Arg Asp Ile Asp  *
                245

TGGATGTTTG GAAACATTTT TTAAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC     828

TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTTGTAGAG     888

AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT     948

TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT    1008

ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC CCCTTCGCAG    1068

CTGAAGTGGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCTT    1128

TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA    1188

TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAATGTTT TCTTTGCAAA    1248

GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGTCTTGCT    1308

GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC    1368

CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCCTAATA TCAAATGCAG    1428

TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAAG CCTGTGCAAA    1488

AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA    1548

TTTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC    1608

TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA    1668

AATTGTACCT TTTTTTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAAA    1728

AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC ATTGCCTTTG    1788

AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC                               1823
```

Figure 1 (continued)

```
Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
 1               5                  10                  15

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
            20                  25                  30

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
        35                  40                  45

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
    50                  55                  60

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
65                  70                  75                  80

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
                85                  90                  95

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
            100                 105                 110

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
        115                 120                 125

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
    130                 135                 140

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
145                 150                 155                 160

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
                165                 170                 175

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
            180                 185                 190

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
        195                 200                 205

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
    210                 215                 220

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
225                 230                 235                 240

Val Arg Asp Ile Asp  *
                245
```

Figure 2

```
CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG GGGGCCGTGG      60

CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC     120

CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG        171
                        Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys
                                    250                 255

TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC        219
Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His
            260                 265                 270

GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA        267
Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro
        275                 280                 285

CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG       315
Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu
    290                 295                 300

GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG       363
Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln
305                 310                 315                 320

ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA       411
Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg
                325                 330                 335

ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG       459
Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu
            340                 345                 350

AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT       507
Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
        355                 360                 365

CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC       555
Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
    370                 375                 380

TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC       603
Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
385                 390                 395                 400

CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT       651
Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
                405                 410                 415

GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG       699
Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
            420                 425                 430

TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC       747
Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
        435                 440                 445

GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC       795
Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
    450                 455                 460

ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT       843
Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
465                 470                 475                 480
```

Figure 3

```
CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT      891
Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
                485                 490                 495

TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT      939
Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn
            500                 505                 510

TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC      987
Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
        515                 520                 525

CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG     1035
Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu
    530                 535                 540

GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC     1083
Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp
545                 550                 555                 560

ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT              1132
Ile Asp  *

TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG    1192

GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG    1252

TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTAA    1312

TGATTTCCTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA    1372

CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA    1432

ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA AGGGTTAAGT    1492

TCTTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTT CTAATGAGGA    1552

GAAAAATATA TGTATTTTTA TATAATGTCT AAAGTTATAT TTCAGGTGTA ATGTTTTCTG    1612

TGCAAAGTTT TGTAAATTAT ATTTGTGCTA TAGTATTTGA TTCAAAATAT TTAAAAATGT    1672

CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTTAACTGG TGCACTTTGT    1732

AATTCCCCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTTCTGGT GACCACATGT    1792

AGTTTATTTC TTTATTCTTT TTAACTTAAT AGAGTCTTCA GACTTGTCAA AACTATGCAA    1852

GCAAAATAAA TAAATAAAAA TAAAATGAAT ACCTTGAATA ATAAGTAGGA TGTTGGTCAC    1912

CAGGTGCCTT TCAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC CAAAAAGGAA    1972

CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA GGTGTCTTTT    2032

TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA AAATGTACTA    2092

TAGTTTATCA GCCAAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT TTATTATACT    2152

GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTTGGT ACAAAAAATA AATTTGTACG    2212

AAAAAAAAAA AAAAAAAAAA AAAAA                                          2237
```

Figure 3 (continued)

```
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1               5                  10                  15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
            20                  25                  30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
        35                  40                  45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
    50                  55                  60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65                  70                  75                  80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
                85                  90                  95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
            100                 105                 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
        115                 120                 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
    130                 135                 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145                 150                 155                 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
                165                 170                 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
            180                 185                 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
        195                 200                 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
    210                 215                 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225                 230                 235                 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
                245                 250                 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
            260                 265                 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
        275                 280                 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
    290                 295                 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  *
305                 310                 315
```

Figure 4

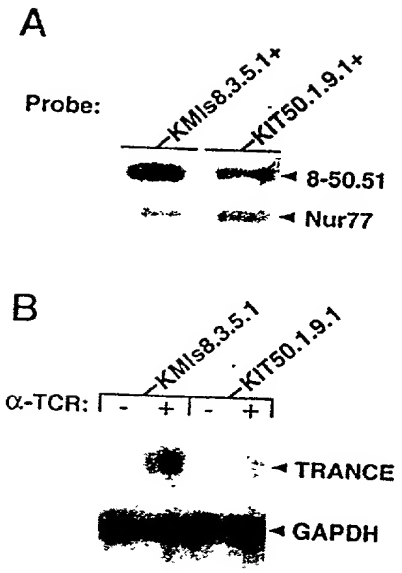
A
Probe:
KMIs8.3.5.1+
KIT50.1.9.1+
8-50.51
Nur77
B
KMIs8.3.5.1
KIT50.1.9.1
α-TCR: - + - +
TRANCE
GAPDH

Figure 5

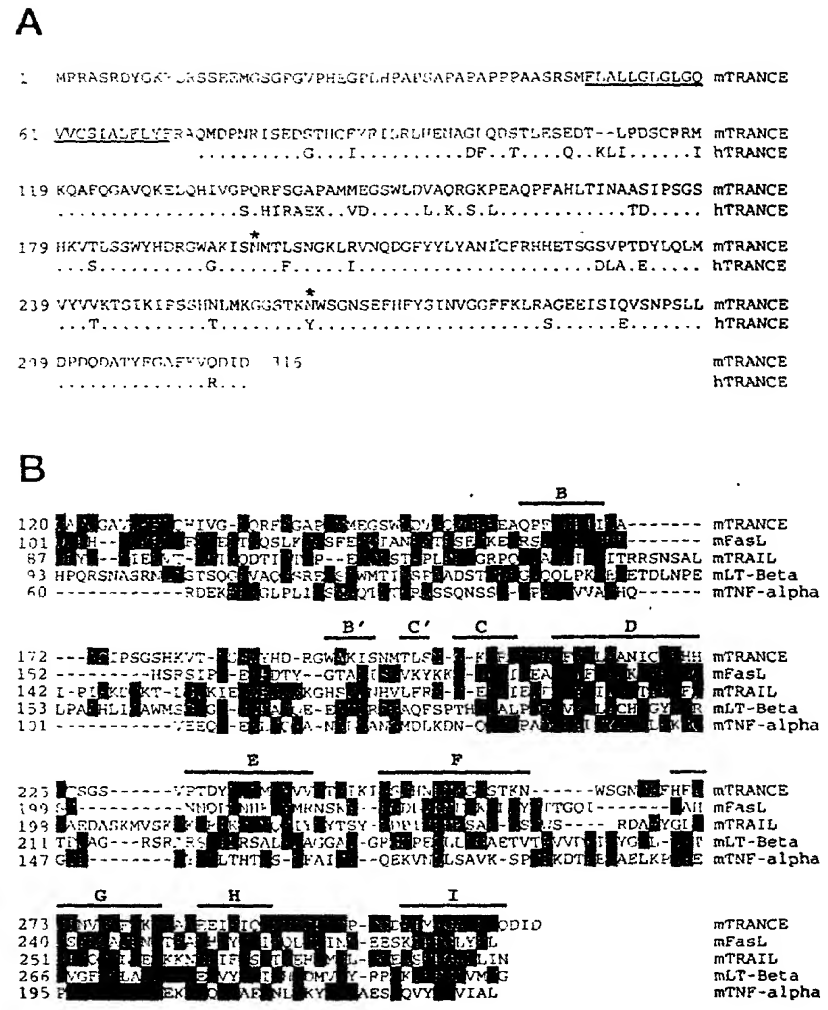
A
B
B
B′
C′
C
D
E
F
G
H
I
mTRANCE
mFasL
mTRAIL
mLT-Beta
mTNF-alpha
hTRANCE

Figure 6

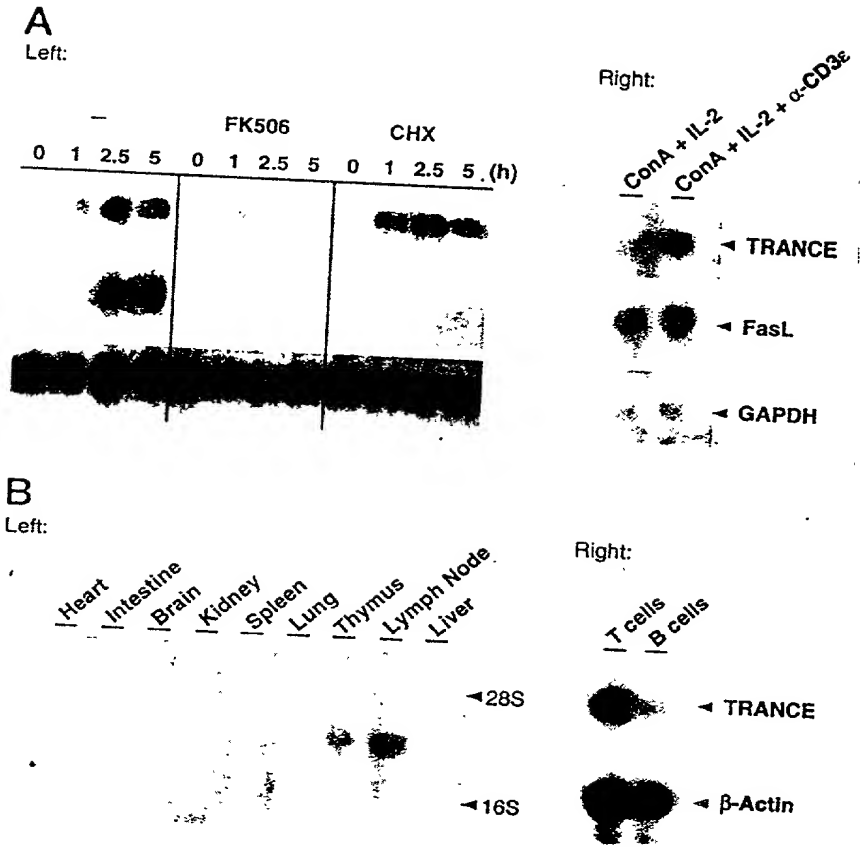
A
Left:
–
FK506
CHX
0 1 2.5 5 0 1 2.5 5 0 1 2.5 5 (h)
Right:
ConA + IL-2
ConA + IL-2 + α-CD3ε
TRANCE
FasL
GAPDH
B
Left:
Heart
Intestine
Brain
Kidney
Spleen
Lung
Thymus
Lymph Node
Liver
28S
16S
Right:
T cells
B cells
TRANCE
β-Actin

Figure 7

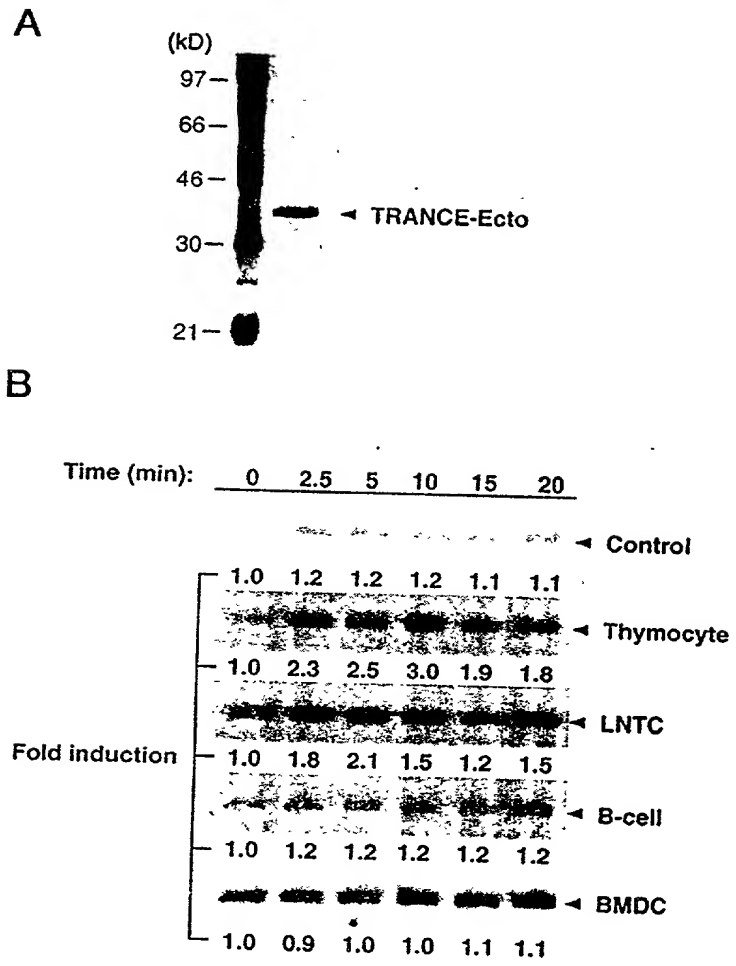
A
(kD)
97
66
46
30
21
TRANCE-Ecto
B
Time (min): 0 2.5 5 10 15 20
Control
1.0 1.2 1.2 1.2 1.1 1.1
Thymocyte
1.0 2.3 2.5 3.0 1.9 1.8
LNTC
Fold induction
1.0 1.8 2.1 1.5 1.2 1.5
B-cell
1.0 1.2 1.2 1.2 1.2 1.2
BMDC
1.0 0.9 1.0 1.0 1.1 1.1

Figure 8

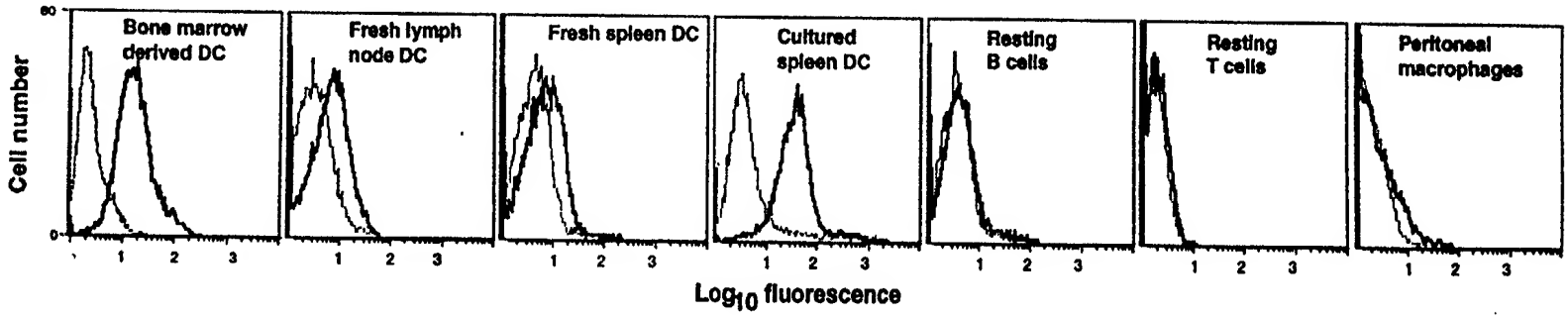
Cell number
60
0
Bone marrow derived DC
Fresh lymph node DC
Fresh spleen DC
Cultured spleen DC
Resting B cells
Resting T cells
Peritoneal macrophages
1 2 3
Log10 fluorescence

Figure 9

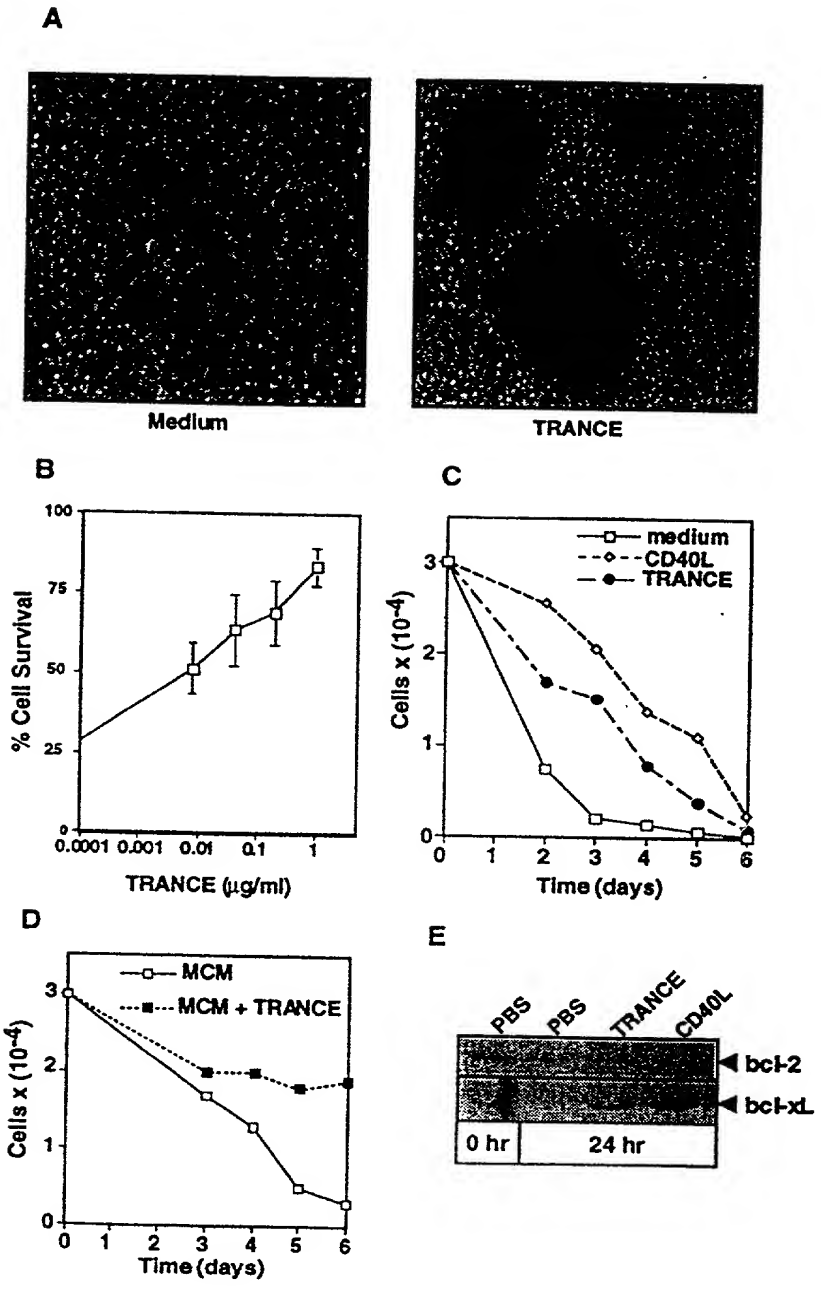
A
Medium
TRANCE
B
% Cell Survival
TRANCE (µg/ml)
C
medium
CD40L
TRANCE
Cells x (10⁻⁴)
Time (days)
D
MCM
MCM + TRANCE
Cells x (10⁻⁴)
Time (days)
E
PBS
PBS
TRANCE
CD40L
bcl-2
bcl-xL
0 hr
24 hr

Figure 10

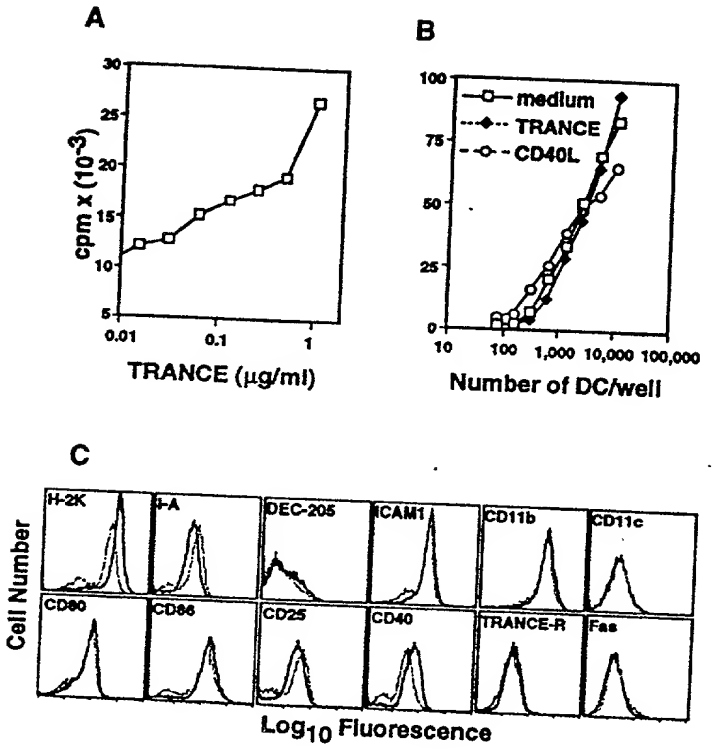
A
cpm x (10^{-3})
30
25
20
15
10
5
0.01
0.1
1
TRANCE (μg/ml)
B
100
75
50
25
0
medium
TRANCE
CD40L
10
100
1,000
10,000
100,000
Number of DC/well
C
Cell Number
H-2K
I-A
DEC-205
ICAM1
CD11b
CD11c
CD80
CD86
CD25
CD40
TRANCE-R
Fas
Log_{10} Fluorescence

Figure 11

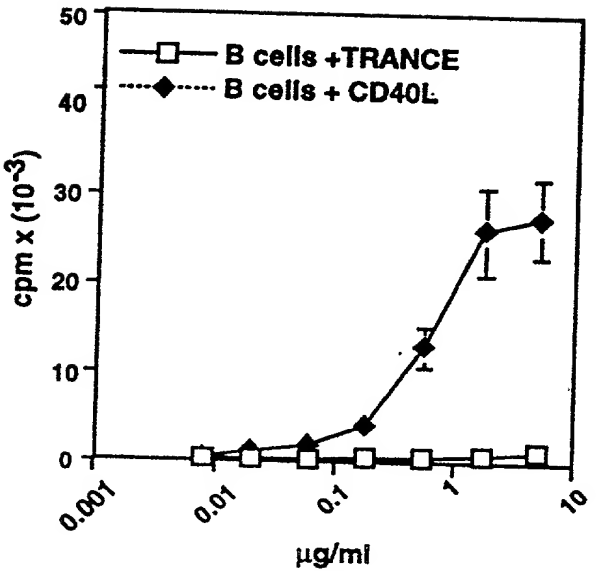
B cells +TRANCE
B cells + CD40L
cpm x (10^{-3})
50
40
30
20
10
0
0.001
0.01
0.1
1
10
µg/ml

Figure 12

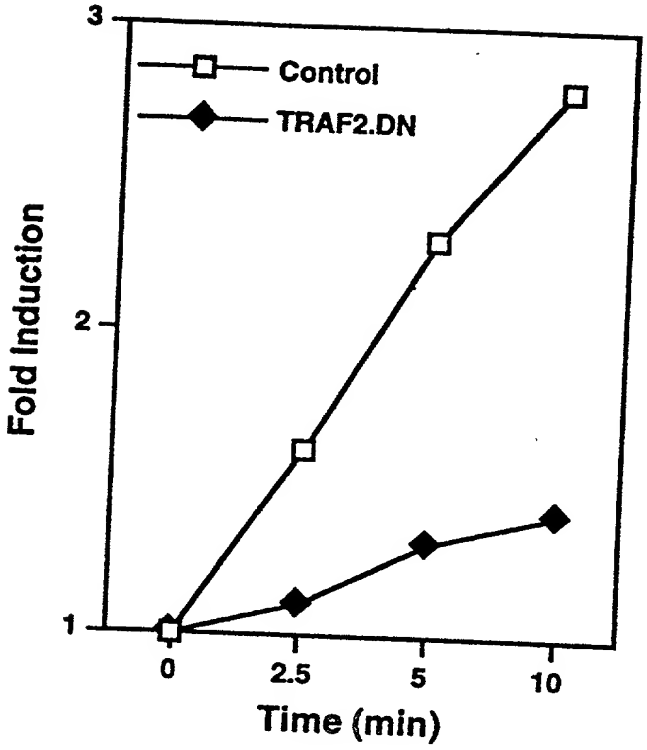

Figure 13

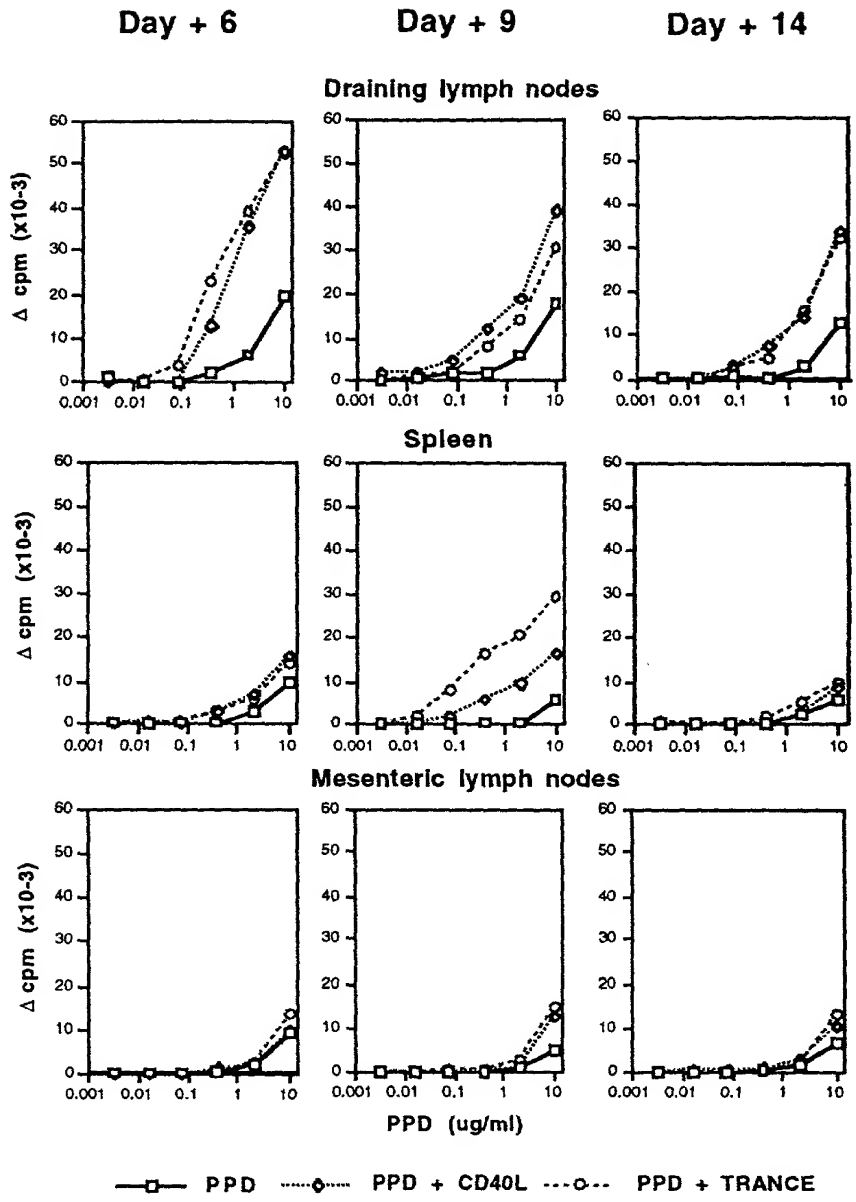
Day + 6
Day + 9
Day + 14
Draining lymph nodes
Spleen
Mesenteric lymph nodes
Δ cpm (x10-3)
PPD (ug/ml)
PPD
PPD + CD40L
PPD + TRANCE

Figure 14

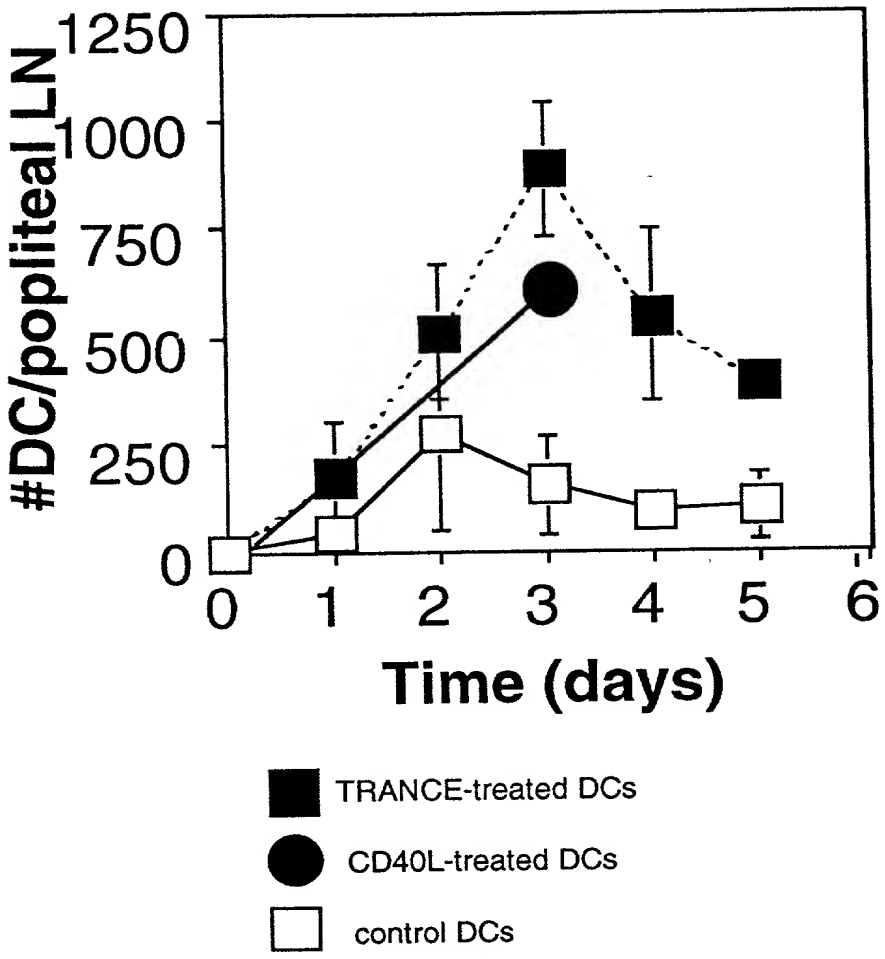
#DC/popliteal LN
1250
1000
750
500
250
0
0
1
2
3
4
5
6
Time (days)
TRANCE-treated DCs
CD40L-treated DCs
control DCs

Figure 15

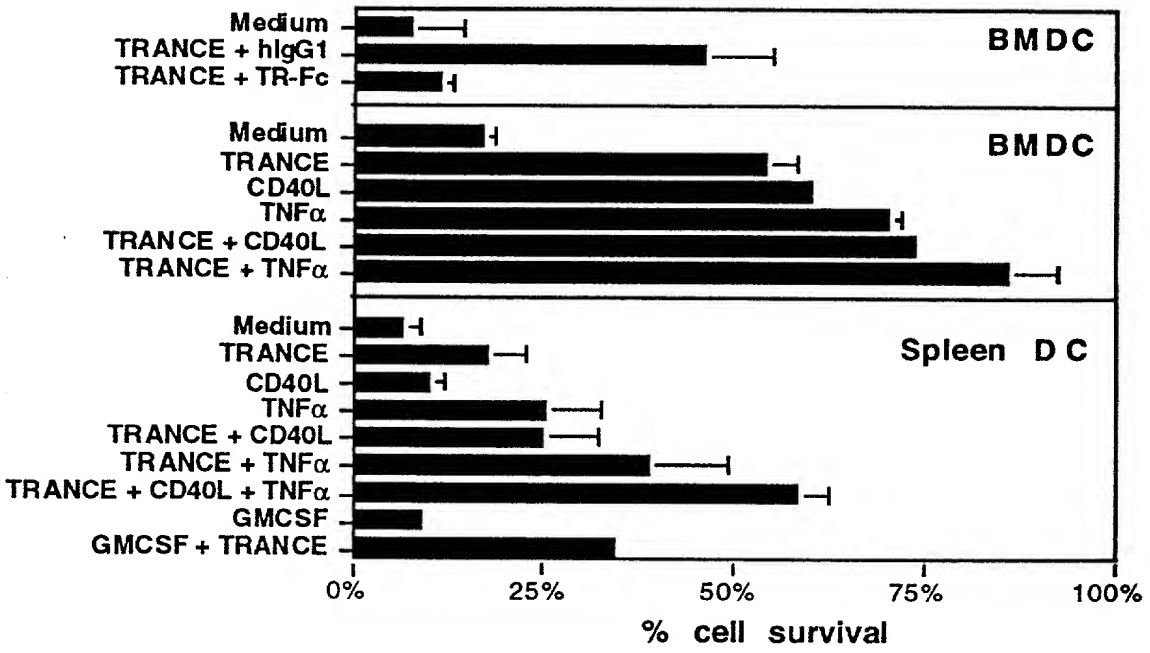
Medium
TRANCE + hIgG1
TRANCE + TR-Fc
BMDC
Medium
TRANCE
CD40L
TNFα
TRANCE + CD40L
TRANCE + TNFα
BMDC
Medium
TRANCE
CD40L
TNFα
TRANCE + CD40L
TRANCE + TNFα
TRANCE + CD40L + TNFα
GMCSF
GMCSF + TRANCE
Spleen DC
0%
25%
50%
75%
100%
% cell survival

Figure 16

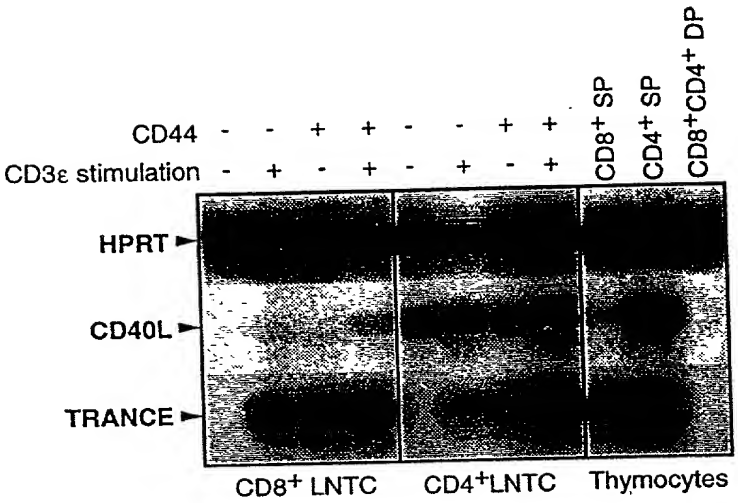
CD44 - - + + - - + +
CD3ε stimulation - + - + - + - +
CD8+ SP
CD4+ SP
CD8+CD4+ DP
HPRT
CD40L
TRANCE
CD8+ LNTC
CD4+LNTC
Thymocytes

Figure 17

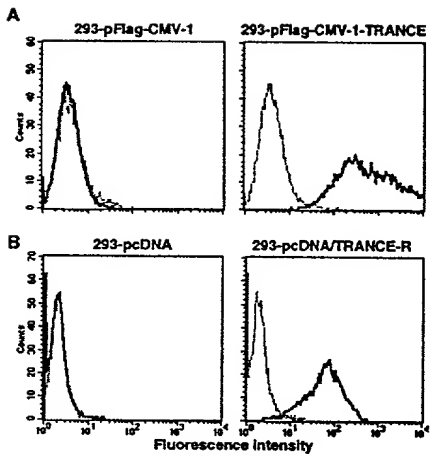
A
293-pFlag-CMV-1
293-pFlag-CMV-1-TRANCE
B
293-pcDNA
293-pcDNA/TRANCE-R
Fluorescence Intensity

Figure 18

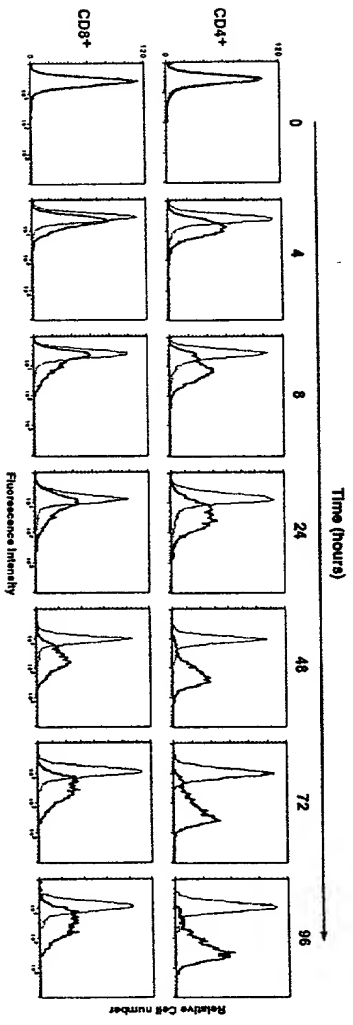
CD8+
CD4+
0
4
8
24
48
72
96
Time (hours)
Fluorescence Intensity
Relative Cell number

Figure 19

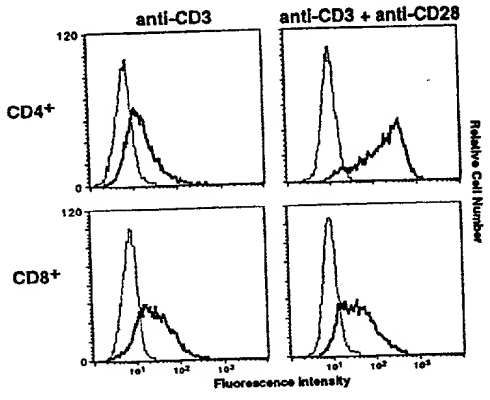
anti-CD3
anti-CD3 + anti-CD28
CD4+
CD8+
120
0
Relative Cell Number
Fluorescence Intensity

Figure 20

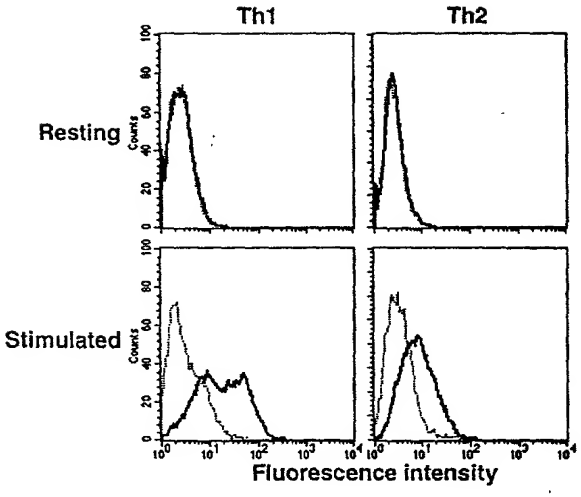
Th1
Th2
Resting
Stimulated
Counts
Fluorescence intensity

Figure 21

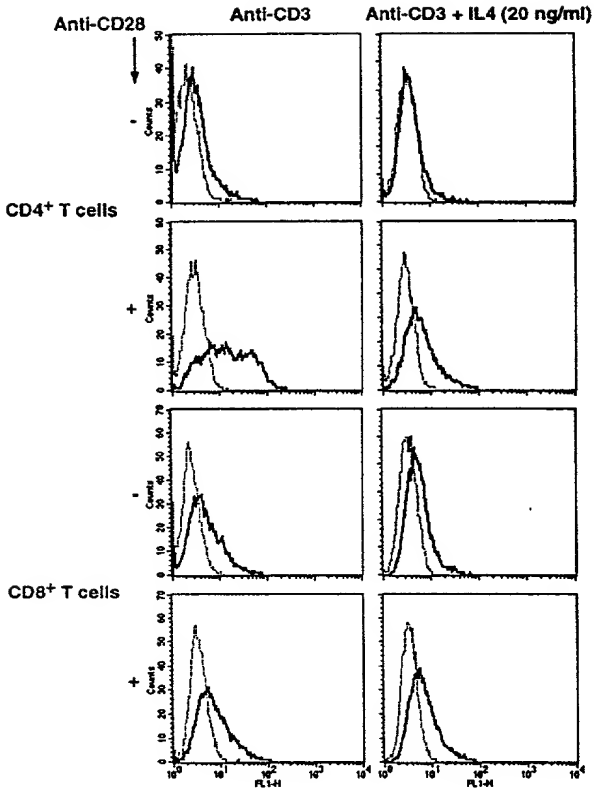
Anti-CD28
Anti-CD3
Anti-CD3 + IL4 (20 ng/ml)
CD4+ T cells
CD8+ T cells
-
+
-
+
Count
FL1-H

Figure 22

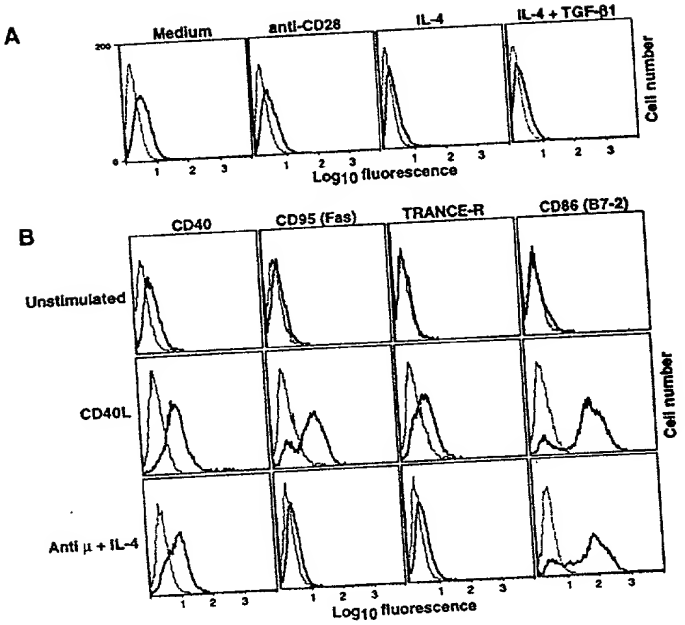
A
Medium
anti-CD28
IL-4
IL-4 + TGF-β1
200
0
1 2 3
Cell number
Log10 fluorescence
B
CD40
CD95 (Fas)
TRANCE-R
CD86 (B7-2)
Unstimulated
CD40L
Anti μ + IL-4
Cell number
Log10 fluorescence

Figure 23

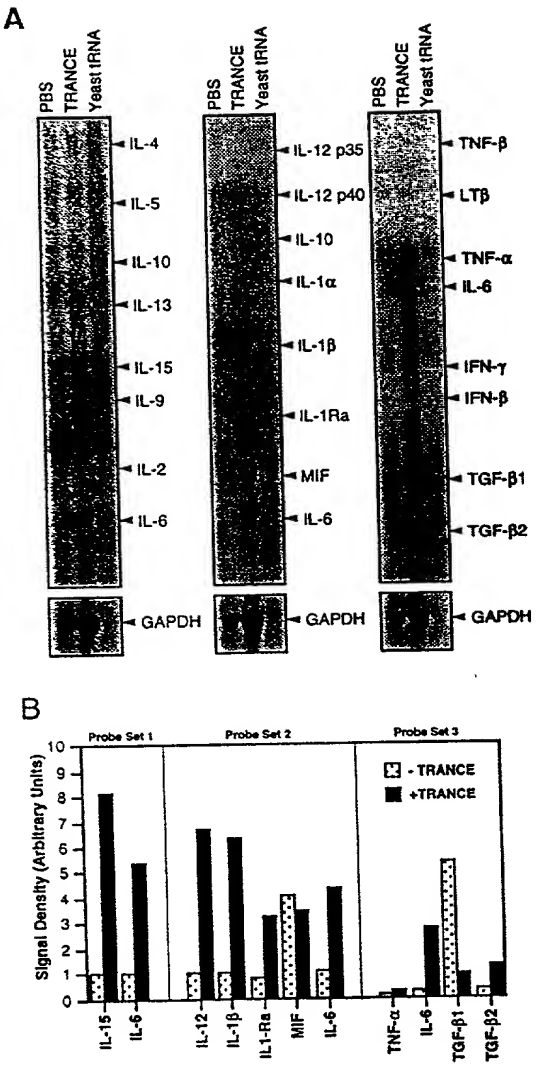
A
PBS
TRANCE
Yeast tRNA
IL-4
IL-5
IL-10
IL-13
IL-15
IL-9
IL-2
IL-6
GAPDH
IL-12 p35
IL-12 p40
IL-10
IL-1α
IL-1β
IL-1Ra
MIF
IL-6
GAPDH
TNF-β
LTβ
TNF-α
IL-6
IFN-γ
IFN-β
TGF-β1
TGF-β2
GAPDH
B
Probe Set 1
Probe Set 2
Probe Set 3
- TRANCE
+TRANCE
Signal Density (Arbitrary Units)
IL-15
IL-6
IL-12
IL-1β
IL1-Ra
MIF
IL-6
TNF-α
IL-6
TGF-β1
TGF-β2

Figure 24